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**RAW SEQUENCE LISTING** DATE: 01/23/2002  
**PATENT APPLICATION:** US/09/865,363 TIME: 09:53:48

Input Set : N:\Crf3\RULE60\09865363.raw.txt  
Output Set: N:\CRF3\01232002\I865363.raw

## **SEQUENCE LISTING**



**ENTERED**

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65	(ii) MOLECULE TYPE: cDNA	
67	(iii) HYPOTHETICAL: NO	
69	(iv) ANTI-SENSE: NO	
71	(vi) ORIGINAL SOURCE:	
72	(A) ORGANISM: HOMO SAPIENS	
74	(vii) IMMEDIATE SOURCE:	
75	(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS	
76	(B) CLONE: 9D-8A	
78	(ix) FEATURE:	
79	(A) NAME/KEY: CDS	
80	(B) LOCATION: 93..1868	
83	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
85	GCTGCTGCTG CTCTGGCGCG TGCTCGCCCC GCTGCAGTTT TATCCAGAAA GAGCTGTGTG	60
87	GACTCTCTGC CTGACCTTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT	113
88	Val Ala Leu Gln Ile Ala Pro	
89	1 5	
91	CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC	161
92	Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn	
93	10 15 20	
95	AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT	209
96	Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Ser	
97	25 30 35	
99	GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG	257
100	Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp	
101	40 45 50 55	
103	AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG	305
104	Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys	
105	60 65 70	
107	GCC CTG GTG GCC GTG GTC GCC AAC AGC ACG ACC CCC CGG CGC TGC	353
108	Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys	
109	75 80 85	
111	GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC	401
112	Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg	
113	90 95 100	
115	CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG	449
116	Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln	
117	105 110 115	
119	CTC AAC AAG GAC ACA GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT	497
120	Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser	
121	120 125 130 135	
123	GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC	545
124	Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr	
125	140 145 150	
127	TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG	593
128	Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala	
129	155 160 165	
131	GTT TGC AGT TCT TCT CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT	641
132	Val Cys Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His	
133	170 175 180	

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135	GTT TAC TTG CCC GGT TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC	689
136	Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Phe Ala Ser Val Ala	
137	185 190 195	
139	CTG GTG GCT GCC ATC ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA	737
140	Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys	
141	200 205 210 215	
143	GCA CTC ACA GCT AAT TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC	785
144	Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg	
145	220 225 230	
147	CTA AGT GGA GAT AAG GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC	833
148	Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His	
149	235 240 245	
151	ACG GCA AAC TTT GGT CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG	881
152	Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu	
153	250 255 260	
155	ACT CTG GAG GAG AAG ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA	929
156	Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln	
157	265 270 275	
159	GGT GGT GTC TGT CAG GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA	977
160	Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln	
161	280 285 290 295	
163	GGC GAA GAT GCC AGG ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG	1025
164	Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu	
165	300 305 310	
167	GAA GAC AGC TTC AGA CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG	1073
168	Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg	
169	315 320 325	
171	CCC TCC CAG CCC ACA GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC	1121
172	Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser	
173	330 335 340	
175	AAA TCC ACA CCT CCT TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC	1169
176	Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp	
177	345 350 355	
179	AGT TTA AGC CAG TGC TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA	1217
180	Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu	
181	360 365 370 375	
183	AGC TGC AAC TGC ACT GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG	1265
184	Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met	
185	380 385 390	
187	TCC TCT GAA AAC TAC TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG	1313
188	Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro	
189	395 400 405	
191	CAC TGG GCA GCC AGC CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC	1361
192	His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly	
193	410 415 420	
195	TGC CGG AAC CCT CCT GGG GAG GAC TGT GAA CCC CTC GTG GGT TCC CCA	1409
196	Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro	
197	425 430 435	
199	AAA CGT GGA CCC TTG CCC CAG TGC GCC TAT GGC ATG GGC CTT CCC CCT	1457

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200	Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro	
201	440 445 450 455	
203	GAA GAA GCC AGC AGG ACG GAG GCC AGA GAC CAG CCC GAG GAT GGG	1505
204	Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly	
205	460 465 470	
207	GCT GAT GGG AGG CTC CCA AGC TCA GCG AGG GCA GGT GCC GGG TCT GGA	1553
208	Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly	
209	475 480 485	
211	AGC TCC CCT GGT GGC CAG TCC CCT GCA TCT GGA AAT GTG ACT GGA AAC	1601
212	Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn	
213	490 495 500	
215	AGT AAC TCC ACG TTC ATC TCC AGC GGG CAG GTG ATG AAC TTC AAG GGC	1649
216	Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly	
217	505 510 515	
219	GAC ATC ATC GTG GTC TAC GTC AGC CAG ACC TCG CAG GAG GGC GCG GCG	1697
220	Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala	
221	520 525 530 535	
223	GCG GCT GCG GAG CCC ATG GGC CGC CCG GTG CAG GAG GAG ACC CTG GCG	1745
224	Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala	
225	540 545 550	
227	CGC CGA GAC TCC TTC GCG GGG AAC GGC CCG CGC TTC CCG GAC CCG TGC	1793
228	Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys	
229	555 560 565	
231	GGC GGC CCC GAG GGG CTG CGG GAG CCG GAG AAG GCC TCG AGG CCG GTG	1841
232	Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val	
233	570 575 580	
235	CAG GAG CAA GGC GGG GCC AAG GCT TGA GCGCCCCCA TGGCTGGAG	1888
236	Gln Glu Gln Gly Gly Ala Lys Ala	
237	585 590	
239	CCCGAAGCTC GGAGCCAGGG CTCGCGAGGG CAGCACCGCA GCCTCTGCC CAGCCCCGGC	1948
241	CACCCAGGGA TCGATCGGTA CAGTCGAGGA AGACCACCCG GCATTCTCTG CCCACTTTGC	2008
243	CTTCCAGGAA ATGGGCTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCCA TGCCCACGGA	2068
245	TGCTCAGCAG CCCGCCGCAC TGGGGCAGAT GTCTCCCCTG CCACTCCTCA AACTCGCAGC	2128
247	AGTAATTGTT GGCACTATGA CAGCTATTG TATGACTATC CTGTTCTGTG GGGGGGGGGT	2188
249	CTATGTTTC CCCCCATATT TGTATTCTT TTCATAACTT TTCTTGATAT CTTTCCTCCC	2248
251	TCTTTTTAA TGTAAAGGTT TTCTCAAAA TTCTCCTAAA GGTGAGGGTC TCTTTCTTT	2308
253	CTCTTTCTT TTTTTTTTC TTTTTTGCG AACCTGGCTC TGGCCCAGGC TAGAGTGCAG	2368
255	TGGTGCAGATT ATAGCCCGGT GCAGCCTCTA ACTCCTGGGC TCAAGCAATC CAAGTGTATCC	2428
257	TCCCCACCTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGCCACGCC AGCTTCTCC	2488
259	CCCCGACTCC CCCCCCCCCAG AGACACGGTC CCACCATGTT ACCCAGCCTG GTCTCAAAC	2548
261	CCCCAGCTAA AGCAGTCCTC CAGCCTCGGC CTCCCAAAGT ACTGGGATTA CAGGCAGTGAG	2608
263	CCCCCACGCT GGCCCTGCTT ACGTATTTC TTTTGTGCC CTGCTCACAG TGTTTAGAG	2668
265	ATGGCTTCC CAGTGTGTGT TCATTGTAAA CACTTTGGG AAAGGGCTAA ACATGTGAGG	2728
267	CCTGGAGATA GTTGCTAAAGT TGCTAGGAAC ATGTGGTGGG ACTTTCATAT TCTGAAAAAT	2788
269	GTTCTATATT CTCATTTTC TAAAAGAAAG AAAAAGGAA ACCCGATTTA TTTCTCTGA	2848
271	ATCTTTTAA GTTGTGTGTC TTCCCTAACG AGAACTAACG TCAGTATGTG ACCTTACCCG	2908
273	CTAGGGGGTT AATTATCCA TGCTGGCAGA GGCACACTCAGG TACTTGGTAA GCAAATTCT	2968
275	AAAACCTCAA GTTGCAG CTTGGCATTG TTCTTATTCT AGAGGTCTCT CTGAAAAGA	3028
277	TGGAGAAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGAA GTTCAAGGAA	3088

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279 GAATAAAGTT GAAATTTAA AAAAAAA 3115  
 282 (2) INFORMATION FOR SEQ ID NO: 2:  
 284 (i) SEQUENCE CHARACTERISTICS:  
 285 (A) LENGTH: 591 amino acids  
 286 (B) TYPE: amino acid  
 287 (D) TOPOLOGY: linear  
 289 (ii) MOLECULE TYPE: protein  
 291 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 293 Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu  
 294 1 5 10 15  
 296 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser  
 297 20 25 30  
 299 Ser Lys Cys Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro  
 300 35 40 45  
 302 Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His  
 303 50 55 60  
 305 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn  
 306 65 70 75 80  
 308 Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser  
 309 85 90 95  
 311 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu  
 312 100 105 110  
 314 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro  
 315 115 120 125  
 317 Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys  
 318 130 135 140  
 320 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His  
 321 145 150 155 160  
 323 Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg  
 324 165 170 175  
 326 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu  
 327 180 185 190  
 329 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val  
 330 195 200 205  
 332 Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp  
 333 210 215 220  
 335 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly  
 336 225 230 235 240  
 338 Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala  
 339 245 250 255  
 341 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu  
 342 260 265 270  
 344 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val  
 345 275 280 285  
 347 Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu  
 348 290 295 300  
 350 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr  
 351 305 310 315 320  
 353 Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09865363.raw.txt

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:487 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:537 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:561 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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L:565 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3